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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 29.0089 Seconds
(without alignments) 2457.601 Million cell updates/sec

Title: US-09-807-933B-11

Perfect score: 1895
Sequence: 1 MKFSIIASALLLAASSTYAA.....TFKAVTCPAEIIAKTGCEK 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits/satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

```

STREMBL_21.*
1:  sp_archea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phase.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Query			DB	ID	Description
			Match	Length	Length			
1	1	742.5	39.2	219	14	Q9JH92	Q9jh92 unclassified	
2	2	740.5	39.1	219	14	Q9JH87	Q9jh87 unclassified	
3	3	739.5	39.0	220	14	Q9JH84	Q9jh84 unclassified	
4	4	738.5	39.0	220	14	Q9JH93	Q9jh93 unclassified	
5	5	736.5	38.9	219	14	Q9JH89	Q9jh89 unclassified	
6	6	735.5	38.8	219	14	Q9JH91	Q9jh91 unclassified	
7	7	734.5	38.8	220	14	Q9JH83	Q9jh83 unclassified	
8	8	732.5	38.7	217	14	Q9JH95	Q9jh95 unclassified	
9	9	732.5	38.7	219	14	Q9JH86	Q9jh86 unclassified	
10	10	731.5	38.6	219	14	Q9JH88	Q9jh88 unclassified	
11	11	728.5	38.4	219	14	Q9JH90	Q9jh90 unclassified	
12	12	727.5	38.4	221	14	Q9JH94	Q9jh94 unclassified	
13	13	721.5	38.1	220	14	Q9JH96	Q9jh96 unclassified	
14	14	720	38.0	218	14	Q9JH85	Q9jh85 unclassified	
15	15	692	36.5	410	3	Q9P868	Q9P868 piromyces e	
16	16	654	34.5	305	3	Q9J382	Q9J382 humicola gr	

17	583	30.8	227	3	Q93783	Q93783 humicola gr
18	567	29.9	242	5	Q97401	Q97401 phaedon coc
19	522.5	27.6	271	3	O9UVp3	O9UVp3 alternaria
20	349.5	18.8	112	14	Q9UJH99	Q9UJH99 unclassified
21	346.5	18.4	112	14	Q9UJH40	Q9UJH40 unclassified
22	347.5	18.3	112	14	Q9UJH98	Q9UJH98 unclassified
23	339	17.9	111	14	Q9UJH97	Q9UJH97 unclassified
24	338.5	17.9	112	14	Q9UJH42	Q9UJH42 unclassified
25	336.5	17.8	112	14	Q9UJH41	Q9UJH41 unclassified
26	231.5	12.2	668	5	Q9GY11	Q9GY11 leishmania
27	229.5	12.1	439	3	Q9PB93	Q9PB93 agaricus bi
28	229	12.1	476	3	Q9C1S9	Q9C1S9 humicola in
29	226.5	12.0	493	3	Q9PB8D0	Q9PB8D0 trichoderma
30	225	11.9	439	3	Q92401	Q92401 agaricus bi
31	223	11.8	629	5	Q9N745	Q9N745 leishmania
32	223	11.8	1832	5	Q96503	Q96503 cryptospori
33	220	11.6	648	5	Q9GY33	Q9GY33 leishmania
34	215	11.3	984	5	Q9Y1P7	Q9Y1P7 cryptospori
35	211.5	11.2	704	5	Q9GYA2	Q9GYA2 leishmania
36	210	11.1	572	5	Q9GY37	Q9GY37 leishmania
37	210	11.1	760	5	Q9GYA8	Q9GYA8 leishmania
38	210	11.1	956	5	O00908	O00908 cryptospori
39	208	11.0	327	5	O25334	O25334 leishmania
40	206.5	10.9	371	5	O25333	O25333 leishmania
41	206	10.9	626	5	Q9NDD1	Q9NDD1 leishmania
42	203.5	10.7	197	3	Q9P7F1	Q9P7F1 schizosacch
43	203.5	10.7	197	3	O26878	O26878 trypanosoma
44	202.5	10.7	232	5	O27423	O27423 drosophila
45	201.5	10.6	165	5	O26877	O26877 trypanosoma

ALIGNMENTS

RESULT 1

Q9JH92	PRELIMINARY;	PRT;	219 AA.
ID	Q9JH92		
AC	Q9JH92;		
AD	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation)		
DE	Family 45 cellulase homologue.		
OS	Unclassified eukaryotes.		
OC	Eukaryota.		
OX	NCBI_TaxID=42452;		
NP	[1]		
RN	SEQUENCE FROM N.A.		
RA	Ohtoko K., Ohkumä M., Moriya S., Kudo T.;		
RT	"Diverse genes of family 45 cellulase homolo-		
RT	proteins in the hindgut of termite Reticuliter-		
RL	submitted (JUN-2000) to the EMBL/GenBank/DB-		
RL	EMBL; AB045171; HAA98041.1; -		
DR	HSSP; P43316; 2ENG.		
DR	InterPro; IPR000334; GH_45.		
DR	Pfam; PF02015; Glyco_hydro_45; 1.		
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOW-		
SO	SEQUENCE 219 AA; 23001 MW; 5F2EB81A6DE92		

	Query Match	39.2%	Score 742.5	DB 14	Length 219
	Best Local Similarity	62.8%	Pred. No. 3.9e-45		
	Matches 130	Conservative 24	Mismatches 50	Indels 3	Gaps 2
y	141	ESGNGRTTYRNDCKPSCAWDGKASVTPVLVTCAXDGVSRLGSD--VSGCVGGGAYMCN	198		
b	13	FDGSGRTTYRNDCCASCAWEKAAVTPQVDFCGKDGTTIRVASNDITVXACDGGEGYMCY	72		
y	199	DNQPVWVNDLAYGFPAAASLGSAGASAFCCGCGYELTFTNTAVAGKKFVVQVVTNTGGDLS	258		
b	73	DQAPWAVDVSAYGFAAAC-CGEGSACCNCYELTFTSGPVPNGKKWVVQVVTNTGGDLS	131		
y	259	NHFIDLQMGEGGVYNGCOSQNTNTDNGARYGIGSIISBCDKLPTLOAQGCKWRFPWF	318		
b	132	NQFDLAIFFGGVGIYNGCTQTQSGADPADGWRGYGVGVSRRSECSQLPSGLQAGCWRRFPWF	191		

QY	319	KNADNPEVTFKAVTCAPIIAKTGCR	345
Db	192	QNADNPSINFNVQTCFGLTAKTNCR	218
RESULT 2			
ID	Q9JH87	PRELIMINARY;	PRT; 219 AA.
AC	Q9JH87	SEQUENCE FROM N.A.	
DT	01-OCT-2000	(TrEMBLrel. 15, Created)	
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)	
DE	Family 45 cellulase homologue.		
OS	Unclassified eukaryotes.		
OC	Eukaryota.		
OX	NCBI_TaxID=42452;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ohtoko K., Ohkuma M., Moriya S., Kudo T.;		
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic protists in the hindgut of termite Reticulitermes speratus.";		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB045176; BAA98046.1; -		
DR	HSSP; P43316; 2ENG.		
DR	InterPro; IPR000334; GH 45.		
DR	Pfam; PF02015; Glyco_hydro_45; 1.		
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.		
SQ	SEQUENCE	219 AA; 23134 MW; 48DEF4EC9ACC772D CRC64;	
Query Match			
Best Local Similarity 39.1%; Score 740.5; DB 14; Length 219;			
Matches 130; Conservative 29; Mismatches 49; Indels 3; Gaps 2;			
QY	137	ISGFGSGNRTTRYWDCCKPSCAWDGKASVTKPVLTCADGVSRIGSD--VOSCGVGQA	194
Db	9	ISWSLADSGRTTRYWDCCKPSCGWEKKANVDKPIDTCAKGGTTTAVASNDTVKSCDGDG	68
QY	195	YMCNDNQPVVNDLALYGAFAASLGSAGASAFCCGCVLTFTNTAVAGKFFVQVNTG	254
Db	69	FMCDQTPWQVSDLSUSYGFAAAC--CGGESACCCGCVLTFTSGPVNGKXVQITNG	127
QY	255	DLSTNHFLOMPGGGVYFNGCQSQWNTTNGWARYGGISSECDKLPOLQAGCKWR	314
Db	128	DLGNSQFDLAIPIGGGVGIYNGCTAQSGAPSDGWSRYGGVSSRSECSQLPSGLQAGCWR	187
QY	315	FGWFKNADNPEVTFKAVTCAPIIAKTGCR	345
Db	188	FDWFQADNPSINFQSVCPSEIIAKTNCNR	218
RESULT 3			
ID	Q9JH84	PRELIMINARY;	PRT; 220 AA.
AC	Q9JH84	SEQUENCE FROM N.A.	
DT	01-OCT-2000	(TrEMBLrel. 15, Created)	
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)	
DE	Family 45 cellulase homologue.		
OS	Unclassified eukaryotes.		
OC	Eukaryota.		
OX	NCBI_TaxID=42452;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ohtoko K., Ohkuma M., Moriya S., Kudo T.;		
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic protists in the hindgut of termite Reticulitermes speratus.";		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB045179; BAA98049.1; -		
DR	HSSP; P43316; 2ENG.		
DR	InterPro; IPR000334; GH 45.		
DR	Pfam; PF02015; Glyco_hydro_45; 1.		
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.		
Query Match			
Best Local Similarity 39.0%; Score 738.5; DB 14; Length 220;			
Matches 130; Conservative 25; Mismatches 49; Indels 3; Gaps 2;			
QY	141	PSNGRTRYWDCCKPSCAWDGKASVTKPVLTCADGVSRIGSD--VOSCGVGQA	198
Db	14	FGDTGRTRYWDCCKPSCGWEKKANVDKPIDTCAKGGTTTAVASNDTVKSCDGDG	73
QY	199	DNQPVVNDLALYGAFAASLGSAGASAFCCGCVLTFTNTAVAGKFFVQVNTG	258
Db	74	DQSPGVNDLALYGAFAAAV--SGGESAACCCVLTFTSGPVNGKXVQVNTG	132
QY	259	NHFDLQMPGGGVYFNGCQSQWNTTNGWARYGGISSECDKLPOLQAGCKWR	318
Db	133	NQFDLAIPIGGGVGIYNGCTAQSGAPADGWSRYGGVSSRSECSQLPSGLQAGCWR	192
QY	319	KNADNPEVTFKAVTCAPIIAKTGCR	345
Db	193	QNADNPSINFNVQTCFGLTAKTNCR	219
RESULT 5			
ID	Q9JH89	PRELIMINARY;	PRT; 219 AA.
AC	Q9JH89	SEQUENCE FROM N.A.	
DT	01-OCT-2000	(TrEMBLrel. 15, Created)	

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DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045174; BAA98044.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23033 MW; CA295CAD8F393199 CRC64;

Query Match 38.9%; Score 736.5; DB 14; Length 219;
Best Local Similarity 62.7%; Pred. No. 1e-44;
Matches 128; Conservative 28; Mismatches 45; Indels 3; Gaps 2;

QY 144 NGRTRYWDCCKPSCAWDGKASVTKPVLTCADGVSRRLGSD--VQSGCVGGQAYMCDNQ 201
DB 16 SGKTRYWDCCKGSGWEKKANVDKPIDTCAKDGTRVASNDTVKSGCDGDMCYDQT 75

QY 202 PWVNDLLAYGFAAASLGSAAGAFCCGCGCYELTFTNTAVAGKFFVQVTTGDDISTNH 261
DB 76 PWCVDLSLGYFAAAAC-CGSGGACCGCYELTFTSGPVNGKMWVQITVTTGGDLGSGNQ 134

QY 262 DLQMPGGGVYFNGCQSQWNTNTDGMGARYGGISSISECDKLPQLQAGCKRFGWFKNA 321
DB 135 DLAIPEGGVGIYNGCTAQSAGPADGWSRGVSSRSECSQLPSGLQAGCQWRDWFQNA 194

QY 322 DNEVTFKAVTCPAEIIAKTGCCR 345
DB 195 DNFISNFKVVKCPAEIIAKTNCNR 218

RESULT 6
QYH91 ID QYH91 PRELIMINARY; PRT; 219 AA.
AC QYH91
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045172; BAA98042.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23126 MW; A712EF3FCAB041C CRC64;

Query Match 38.8%; Score 735.5; DB 14; Length 219;
Best Local Similarity 62.1%; Pred. No. 1.2e-44;
Matches 131; Conservative 26; Mismatches 51; Indels 3; Gaps 2;

QY 137 ISGFGNGGTRYWDCCKPSCAWDGKASVTKPVLTCADGVSRRLGSD--VQSGCVGGQ 194
DB 9 ISWILGSGRTRYWDCCKASAKWEKAAVTPQVDTCADKGTTRVASNDTVKSCDGGEG 68

QY 195 YMCNDNQPVVNDLLAYGFAAASLGSAAGAFCCGCGCYELTFTNTAVAGKFFVQVTTG 254

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DB 69 YMCYDQAPWAVNDVSVAYGFAAAAC-CGSGGACCCNYELTFTSGPVNGKMWVQVTTG 127
QY 255 DLSTNHFDLQMPGGGVYFNGCQSQWNTNTDGMGARYGGISSISECDKLPQLQAGCKWR 314
DB 128 DLGSGNQFDLAIPEGGVGIYNGCTAQSAGPADGWSRGVSSRSECSQLPSGLQAGCQWT 187
QY 315 FGMFKNADNPEVTFKAVTCPAEIIAKTGCCR 345
DB 188 FWFQNAENPSINFNOVTCPSSELTAKTNCNR 218

RESULT 7
QYH83 ID QYH83 PRELIMINARY; PRT; 220 AA.
AC QYH83
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045167; EAA98037.1; -
DR EMBL; AB045166; EAA98036.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFA5F3 CRC64;

Query Match 38.8%; Score 734.5; DB 14; Length 220;
Best Local Similarity 61.8%; Pred. No. 1.4e-44;
Matches 128; Conservative 26; Mismatches 50; Indels 3; Gaps 2;

QY 141 FSGNGTRYWDCCKPSCAWDGKASVTKPVLTCADGVSRRLGSD--VQSGCVGGQAYMCMN 198
DB 14 FGDSGKTRYWDCCKGSGWEAKADVSKPIDTCAKDGTRVASNDTVKSGCDGDMCY 73

QY 199 DNQPVVNDLLAYGFAAASLGSAAGAFCCGCGCYELTFTNTAVAGKFFVQVTTGDDIST 258
DB 74 DQTPWGVNDLYALGFAAAAL-SGGEKAAACCCNYELTFTSGPVNGKMWVQVTTGDLGS 132

QY 259 NHFDLQMPGGGVYFNGCQSQWNTNTDGMGARYGGISSISECDKLPQLQAGCKRFGWF 318
DB 133 NQFDLAIPEGGVGIYNGCTAQSAGPADGWSRGVSSRSECSQLPSGLQAGCQWRDWF 192

QY 319 KNADNPEVTFKAVTCPAEIIAKTGCCR 345
DB 193 QNADNPNNFNVVSCPSSELTAKTNCNR 219

RESULT 8
QYH95 ID QYH95 PRELIMINARY; PRT; 217 AA.
AC QYH95
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic

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Db 135 IAIPIGGVGLYNGCTSGAPADGWGSRYGVSRSRSECSQLPSGLQAGCQWRDFWFOAD 194
Qy 323 NPEVTFKAVTCPAEIIAKTCGERK 346
Db 195 NPSITFNEVSCPGDLTSKTCNRQ 218

RESULT 15

Q9P868 Q9P868 PRELIMINARY; PRT; 410 AA.
AC Q9P868;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endoglucanase 45A.
GN CEL45A.
OS Piromyces equi.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimasticeae; Piromyces.
OX NCBI_TaxID=99929;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20391845; PubMed=10931904;
RX Eberhardt R.Y., Gilbert H.J., Hazlewood G.P.;
RA "Primary sequence and enzymatic properties of two modular
RT endoglucanases, Cel5A and Cel45A, from the anaerobic fungus Piromyces
RT equi.";
RL Microbiology 146:1999-2008(2000).
DR EMBL; AJ277482; CAB92325.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR002883; CBD 5.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02013; CBM_10; 3.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 410 AA; 44380 MW; D813BD9CFD8238DC CRC64;

Query Match 36.5%; Score 692; DB 3; Length 410;
Best Local Similarity 37.3%; Pred. No. 2.7e-41;
Matches 155; Conservative 45; Mismatches 125; Indels 90; Gaps 12;
Qy 1 MKFSIIASALLAASSTVAEC---SQYGCGGKMMWTPCTCTSGFTCV-----GAENNE 53
Db 1 MRLATSCIALAASAKVSAACWAQSQGYNC-----NNPSSTKVEYTDASGQWGVQNGQ 55
Qy 54 WYQCIPNDVOQGNPKTTTTTTTAAATTTKAPVT----- 87
Db 56 WCGIDYSYGQNGNESCTGNGSYPCNCTCQATYTDGDDWAFENGWCGIKNSCKQOPON 115
Qy 88 -----TTKATTTT-----TKAPVTTTKATTTTITTTTITTT 120
Db 116 NNQCTGNGAYRCCNTCQATYTDNEGKAFENGWCGIKYSCPSQQTITTTTTRITTTTQ 175
Qy 121 TKAATTTSSNGVSPISGFGSG-NGRTRWDCKPSCAW-----DGKASVTKPVLTC 173
Db 176 QOPTSGGNSNVPLNP--PDFSGQTGKTRYWDCCCLASCWQENCKNDGAQGV---VRSC 230
Qy 174 AKDGVSRIGS-----DVQSGCVGGQAYMCNDNQPVVNDLQYFAAASLGSAGASAFCC 228
Db 231 NVDGITPTDLSNLWRVSGGNGSVYMCNQOPWAINDNVAYGVA-----SHEKCC 283
Qy 229 GCYELTFTNTAVAGKFFVQVNTGDDLSSTNHFDLQMPGGGVGPNCGSQSOWNTNTDQWG 288
Db 284 TCQRLKFTSGPIAGQKIVQTTNTGGDLSSNHFDLQMPGGGFGIPDGCTSQFGGSYQ-WG 342
Qy 289 ARYGGISSISCDKLPLOAGCKWRFGWFKNADNPVEYTKAVTCPAEIIAKTCG 343
Db 343 ERYGGISSASQCANLPQKACGEWRFNFKNADNPVVFERVQCPKELTEITGC 397